

[Home](#)**Paracel BLAST Results**[Help](#)**MEGABLAST 1.2.3-Paracel [2001-11-20]****Reference:**

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),  
 "A greedy algorithm for aligning DNA sequences",  
*J Comput Biol* 2000; 7(1-2):203-14.

**Database:** Homo\_sapiens.latestgp.fa  
 26,679 sequences; 200,800,637,119 total letters

**Query=** 241id3  
 (2853 letters)

Score (bits)	E Value
Sequences producing significant alignments:	
AP002986.2.1.157963	1899 0.0
AP003459.2.1.28000	1528 0.0
AL590714.27.1.133512	64 5e-07
AP001599.1.1.118241	62 2e-06
AP001598.1.1.171038	62 2e-06

>AP002986.2.1.157963  
 Length = 157963

Score = 1899 bits (958), Expect = 0.0  
 Identities = 958/958 (100%)  
 Strand = Plus / Plus

Query: 1 atgcttctgctggcatcctaaccctggcttcgcgcggcgaaaccgctggaggctctgag 60  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 134115 atgcttctgctggcatcctaaccctggcttcgcgcggcgaaaccgctggaggctctgag 134174

Query: 61 ccagagcgggaggtagtcgttccatccactggacccggacattaacggccggcgtac 120  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 134175 ccagagcgggaggtagtcgttccatccactggacccggacattaacggccggcgtac 134234

Query: 121 tactggcggtcccgaggactccggatcaggactcattttcagatcacagcattt 180  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 134235 tactggcggtcccgaggactccggatcaggactcattttcagatcacagcattt 134294

Query: 181 caggaggactttacacctacacgtacgcggatgctcagttttggctccgccttctcc 240  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 134295 caggaggactttacacctacacgtacgcggatgctcagttttggctccgccttctcc 134354

Query: 241 actgagcatctggcgccccctccaggggctcacccgggtcttcagacctgcgcacgc 300  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 134355 actgagcatctggcgccccctccaggggctcacccgggtcttcagacctgcgcacgc 134414

Query: 301 tgcttctattctgggacgtgaacgccgagccggactcgttcgctgtgagccgtgc 360  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 134415 tgcttctattctgggacgtgaacgccgagccggactcgttcgctgtgc 134474

Query: 361      qqqqqqactccqcgqagcctttagctaccgaggcgccgagtatgtcattagccgctgccc 420

124584

Quality: 100%      99.99999999999999%      99.99999999999999%      99.99999999999999%

Query: 601 agtcgttagccggcgcaggctctgggcgcggcaagcgttcgtgttatccccggtaacgtg 660

Query: 661 gagacgcgtgggtcgccgacgaggtaatggtcaagttccacggcgcggacctggAACAT 720

[View Details](#) | [Edit](#) | [Delete](#)

Sequence 721: tatatgtggatgtggaaaggggggggggacttacccggcatcccaggatctcaac, 780

Subjct: 134835 tatctgctgacgctgctggcaacggcgccacttaccgccatcccagcatcctcaac 134

Sbjct: 134895 cccatcaacatcattatggtaaagggtgcgtcttagagatcgtaactccggggccaaag 134

125

Sbjct: 135015 aaagttagtgacaaggccccggacttggacactgccatcccttaccaggcagg 135072

Score = 571 bits (288), Expect = e-160  
Identities = 288/288 (100%)

Strand = Plus / Plus

Strand = Plus / Plus

Query: 1258 ggtgactgcctcctggaccaaccaggcaagccatctccctgccccgaggatctgccgggc 131/

Sbjct: 147637 |||||||ggtgactgcctcctggaccaacccagcaagccatctccctgcccaggatctgccggc 147696

Query: 1318 gccagctacaccctgagccagcagtgcgagctggctttggcgtggctccaaggccctgt 1377

Sbjct: 147697 |||||||gccagctacaccctgagccagcagtgcgagctggctttggcgtggctccaaggccctgt 147756

Query: 1378 ctttacatgcagtaactgcaccaagctgtggtcaccggaaaggccaaggacagatgg 1437

Sbjct: 147757 |||||||ctttacatgcagtaactgcaccaagctgtggtcaccggaaaggccaaggacagatgg 147816

Query: 1438 tgccagaccgcacttccctggccatggcaccagctgtggcgaggcaagctctgc 1497

Sbjct: 147817 tgccagaccgcacttccctggccatggcaccagctgtggcgaggcaagctctgc 147876

Query: 1498 ctcaaaggggcctgcgtggagagacacaacctaacaaggcacagggtg 1545

Sbjct: 147877 |||||||ctcaaaggggcctgcgtggagagacacaacctaacaaggcacagggtg 147924

Score = 371 bits (187), Expect = 2e-99

Identities = 187/187 (100%)

Strand = Plus / Plus

Query: 1719 agcctccggaaagagacttccggaggaggcagtgtgaggcttcaacggctacaaccacag 1778

Sbjct: 156059 |||||||agcctccggaaagagacttccggaggaggcagtgtgaggcttcaacggctacaaccacag 156118

Query: 1779 caccaaccggctcactctgcgcgtggcatgggtgcctaagtactccggcgtgtctcccg 1838

Sbjct: 156119 |||||||caccaaccggctcactctgcgcgtggcatgggtgcctaagtactccggcgtgtctcccg 156178

Query: 1839 ggacaagtgcagactcatctggcggccatggcactggctacttctatgtgctggcacc 1898

Sbjct: 156179 |||||||ggacaagtgcagactcatctggcggccatggcactggctacttctatgtgctggcacc 156238

Query: 1899 caaggtg 1905

Sbjct: 156239 |||||||caaggtg 156245

Score = 355 bits (179), Expect = 1e-94

Identities = 179/179 (100%)

Strand = Plus / Plus

Query: 1901 aggtgggtggacggcacgctgtgctctccctgactccacacctccgtctgtgtccaaggcaagt 1960

Sbjct: 156347 |||||||agggtgggtggacggcacgctgtgctctccctgactccacacctccgtctgtgtccaaggcaagt 156406

Query: 1961 gcatcaaggctggctgtatggAACCTGGCTCCAAGAAGAGATTGACAGACTGTGGGG 2020  
Sbjct: 156407 gcatcaaggctggctgtatggAACCTGGCTCCAAGAAGAGATTGACAGACTGTGGGG 156466

Query: 2021 tgtgtggggagacaataagagctgcaagaaggtaactggactttcaccaagccatg 2079  
Sbjct: 156467 tgtgtggggagacaataagagctgcaagaaggtaactggactttcaccaagccatg 156525

Score = 355 bits (179), Expect = 1e-94  
Identities = 183/184 (99%), Gaps = 1/184 (0%)  
Strand = Plus / Plus

Query: 1537 cacagggtggatggttcctggccaaatggatccatatggccctgtcgacatgt 1596  
Sbjct: 154398 caca-ggtggatggttcctggccaaatggatccatatggccctgtcgacatgt 154456

Query: 1597 ggtggggcgtgcagctggccaggaggcagtgcaccaacccacccctgccaacggggc 1656  
Sbjct: 154457 ggtggggcgtgcagctggccaggaggcagtgcaccaacccacccctgccaacggggc 154516

Query: 1657 aagtactgcaggagtgagggtgaaataccgatccatgtcaatctggagccctgccccagc 1716  
Sbjct: 154517 aagtactgcaggagtgagggtgaaataccgatccatgtcaatctggagccctgccccagc 154576

Query: 1717 tcag 1720  
Sbjct: 154577 tcag 154580

Score = 339 bits (171), Expect = 6e-90  
Identities = 171/171 (100%)  
Strand = Plus / Plus

Query: 1090 ggccacgtgttcaacatgccccatgacaatgtgaaagtctgtgaggagggtttgggaag 1149  
Sbjct: 147227 ggccacgtgttcaacatgccccatgacaatgtgaaagtctgtgaggagggtttgggaag 147286

Query: 1150 ctccgagccaaccacatgatgtcccgaccctcatccagatcgaccgtgccaacccctgg 1209  
Sbjct: 147287 ctccgagccaaccacatgatgtcccgaccctcatccagatcgaccgtgccaacccctgg 147346

Query: 1210 tcagcctgcagtgtgccatcatcaccgacttcctggacagcgggcacggt 1260  
Sbjct: 147347 tcagcctgcagtgtgccatcatcaccgacttcctggacagcgggcacggt 147397

Score = 278 bits (140), Expect = 2e-71

Identities = 143/144 (99%)  
Strand = Plus / Plus

Query: 948 caccaggcaggacctgtgtggagccaccacctgtgacaccctggcatggctatgtggg 1007  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 146620 caccaggcaggacctgtgtggagccaccacctgtgacaccctggcatggctatgtggg 146679

Query: 1008 taccatgtgtgaccccaagagaagactgctctgtcattgaggacatgggcttcatcagc 1067  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 146680 taccatgtgtgaccccaagagaagactgctctgtcattgaggacatgggcttcatcagc 146739

Query: 1068 ct当地actgcccacgagctggg 1091  
||||| ||||| ||||| |||||  
Sbjct: 146740 ct当地actgcccacgagctggg 146763

>AP003459.2.1.28000  
Length = 28000

Score = 1528 bits (771), Expect = 0.0  
Identities = 774/775 (99%)  
Strand = Plus / Plus

Query: 2079 gcatggctacaatttctgtggccatccccgcaggcgcccaacgcatcgacatccgcca 2138  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 3473 gcatggctacaatttctgtggccatccccgcaggcgcccaacgcatcgacatccgcca 3532

Query: 2139 ggcgggttacaaagggtatcgggatgacaactacacctggctctgaagaacagccaagg 2198  
||||| ||||| ||||| ||||| |||||  
Sbjct: 3533 ggcgggttacaaagggtatcgggatgacaactacacctggctctgaagaacagccaagg 3592

Query: 2199 caagtacctgctcaacggcatttcgtgggtcgccggtgagcgggacctgggtgaa 2258  
||||| ||||| ||||| |||||  
Sbjct: 3593 caagtacctgctcaacggcatttcgtgggtcgccggtgagcgggacctgggtgaa 3652

Query: 2259 gggcagtctgctcggtacagcggcacagcgggtggagagcctgcaggctcccg 2318  
||||| ||||| ||||| |||||  
Sbjct: 3653 gggcagtctgctcggtacagcggcacagcgggtggagagcctgcaggctcccg 3712

Query: 2319 gcccatcctggagccgctgaccgtggaggtctccgtggggaaagatgacaccgcccc 2378  
||||| ||||| ||||| |||||  
Sbjct: 3713 gcccatcctggagccgctgaccgtggaggtctccgtggggaaagatgacaccgcccc 3772

Query: 2379 ggtccgctactccttatctgcccaaagagacgcctcgaggacaagtccatccaa 2438  
||||| ||||| ||||| |||||  
Sbjct: 3773 ggtccgctactccttatctgcccaaagagacgcctcgaggacaagtccatccaa 3832

Query: 2439 ggaccccccggggaccctctgtctgcacaacagcgtcctcagccatccaaaccagggtgga 2498  
||||| ||||| ||||| |||||

Sbjct: 3833 ggaccccccgggggaccctctgtcttgacacaatagcgtcctcagcctctccaaccagggtgga 3892

Query: 2499 gcagccggacgacaggccccctgcacgctgggtggctggcagctggggccgtgtccgc 2558

**Start:** 3883 **Stop:** 3952 **Sequence:** ggaggccggaccacggggccctggacactggatggactggagctggggggcgtgtctcccc

Query: 2559 gagctgcggcagtggcttcagaaggccgggtggacttgtcgaaaaatccggccggcaacg 2618

Query: 2019-01-01T00:00:00Z/2019-01-01T23:59:59Z

Query: 2678 atggccacatggagctcaggccgttaccctgttccaaggatgtggaccggggatt 2738

Query: 2739 ccagaggcgccaccggaaagggtttggggccacggaggccggccggccggggaccaggcg 2739

Query: 2799 caacttgcaccgcaaggccccaggagctggacttctgcgtcctgaggccgtgctga 2853

Subject: 4193\_gaacttggacccgaaaggccccaggagctggactttcggtcctaaggccatgtca\_4247

Score = 371 bits (187) Expect = 2e-99

Identities = 187/187 (100%)

Strand = Plus / Plus

Query: 1719 aqcctccqaaaqaccccttccqqqqaqgcaatgtqaggcttcaacggctacaaccacag 1778

[View Details](#) | [Edit](#) | [Delete](#)

Query: 1779 caccAACCGGCTactCTCGCCGTggcatgggtGCCAAGTactCCGGCGTgtctcccccg 1838

Quem: 1838-ccggatccggatctatggggggatggatcgatcttttatgtatggccc 1888

Subject: 1464 ggacaaatgtgcacatcttgcggagccatggcactggcatatccatgtgtgtttggccacc 1525

caaggta

May 1994 - May 2000: Managing Director

Score = 355 bits (179), Expect = 1e+94  
Identities = 179/179 (100%)  
Strand = Plus / Plus

Query: 1901 aggtggacggcacgctgtgtctcactccacccgtctgtgtccaaggcaagt 1960  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 1632 aggtggacggcacgctgtgtctcactccacccgtctgtgtccaaggcaagt 1691

Query: 1961 gcatcaaggctggctgtatggAACCTGGCTCCAAGAAGAGATTGACAGTGTGGGG 2020  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 1692 gcatcaaggctggctgtatggAACCTGGCTCCAAGAAGAGATTGACAGTGTGGGG 1751

Query: 2021 tgtgtggggagacaataagagagctgcaagaaggtaactggactttaccaagccccatg 2079  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 1752 tgtgtggggagacaataagagagctgcaagaaggtaactggactttaccaagccccatg 1810

>AL590714.27.1.133512  
Length = 133512

Score = 63.9 bits (32), Expect = 5e-07  
Identities = 59/68 (86%)  
Strand = Plus / Minus

Query: 955 caggacctgtgtggagccaccacctgtgacaccctggcatggctatgtggtaccatg 1014  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 51486 caggacctgtgtggagtctccacttgcacacgctggatggctatgtggcaccgtc 51427

Query: 1015 tgtgaccc 1022  
||| |||  
Sbjct: 51426 tgtgaccc 51419

>AP001599.1.1.118241  
Length = 118241

Score = 61.9 bits (31), Expect = 2e-06  
Identities = 43/47 (91%)  
Strand = Plus / Minus

Query: 1839 ggacaagtgcAAAGCTCATCTGCCAGCCAAATGGCACTGGCTACTTCT 1885  
||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 42122 ggacagggtgcAAAGCTCATCTGCCAAAGCCAAAGGATTGGCTACTTCT 42076

Score = 48.1 bits (24), Expect = 0.031  
Identities = 30/32 (93%)  
Strand = Plus / Minus

Query: 1450 cacttcccctggccatggcaccagctgtgg 1481

Sbjct: 42840 cacttcccggtgggccccatggcaccaggctgtgg 42809

>AP001598.1.1.171038  
Length = 171038

Score = 61.9 bits (31), Expect = 2e-06  
Identities = 43/47 (91%)  
Strand = Plus / Minus

Query: 1839 ggacaagtgc~~aag~~ctcatctg~~cc~~gagccaa~~tgg~~cactggctacttct 1885  
Sbjct: 163850 ggacagg~~gt~~gc~~aag~~ctcatctg~~cc~~aa~~gg~~cattggctacttct 163804

Score = 48.1 bits (24), Expect = 0.031  
Identities = 30/32 (93%)  
Strand = Plus / Minus

Query: 1450 cacttccccgtgggccgatggcaccagctgtgg 1481  
          ||||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 164568 cacttccccgtggccggatggcaccagctgtgg 164537

Database: Homo\_sapiens.latestgp.fa  
Posted date: Jul 8, 2003 12:51 PM  
Number of letters in database: 200,800,637,119  
Number of sequences in database: 26,679

Lambda	K	H
1.37	0.711	1.31

Gapped			
Lambda	K	H	
1.37	0.711	1.31	

```
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 0, Extension: 0
Number of Hits to DB: 0
length of query: 5708
length of database: 200,800,637,119
effective HSP length: 22
effective length of query: 2831
effective search space used: 0
T: 0
A: 0
X1: 0 ( 0.0 bits)
X2: 20 (39.6 bits)
S1: 12 (24.3 bits)
S2: 24 (48.1 bits)
```